

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/533,176  
Source: P4/10  
Date Processed by STIC: 5/12/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 05/12/2005

PATENT APPLICATION: US/10/533,176

TIME: 08:25:16

Input Set : D:\1392-10-20-PCT.ST25.txt

Output Set: N:\CRF4\05122005\J533176.raw

3 <110> APPLICANT: Syngenta Participations, AG  
 4 Cooper, Bret  
 6 <120> TITLE OF INVENTION: STRESS-RELATED POLYPEPTIDES AND USES THEREFOR  
 8 <130> FILE REFERENCE: 1392-10-20 PCT  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/533,176  
 C--> 10 <141> CURRENT FILING DATE: 2005-04-29  
 10 <150> PRIOR APPLICATION NUMBER: US 60/436,564  
 11 <151> PRIOR FILING DATE: 2002-12-26  
 13 <160> NUMBER OF SEQ ID NOS: 174  
 15 <170> SOFTWARE: PatentIn version 3.2  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 1383  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Oryza sativa  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: CDS  
 25 <222> LOCATION: (1)..(1383)  
 27 <400> SEQUENCE: 1  
 28 gct tcc ttt cgg act gtt ggt gct aaa atc act cag gaa act ggt gat 48  
 29 Ala Ser Phe Arg Thr Val Gly Ala Lys Ile Thr Gln Glu Thr Gly Asp  
 30 1 5 10 15  
 32 ttc ttt gtt agc gat gca gag ggt gac cca gac aaa cca act gat ggt 96  
 33 Phe Phe Val Ser Asp Ala Glu Gly Asp Pro Asp Lys Pro Thr Asp Gly  
 34 20 25 30  
 36 ttt tcc tct att gat gag gct ata ggc gca ttg cat gaa gga aag ttt 144  
 37 Phe Ser Ser Ile Asp Glu Ala Ile Gly Ala Leu His Glu Gly Lys Phe  
 38 35 40 45  
 40 gtt att gct gta gat gat gaa agc ggt gat aat gaa ggg gat ctt gtc 192  
 41 Val Ile Ala Val Asp Asp Glu Ser Gly Asp Asn Glu Gly Asp Leu Val  
 42 50 55 60  
 44 atg gca gct acg ctg gca gac cca gaa tct att gca ttc atg atc agg 240  
 45 Met Ala Ala Thr Leu Ala Asp Pro Glu Ser Ile Ala Phe Met Ile Arg  
 46 65 70 75 80  
 48 aat ggt tct ggg atc atc tca gtg ggc atg aag gaa gag gac tta aca 288  
 49 Asn Gly Ser Gly Ile Ile Ser Val Gly Met Lys Glu Glu Asp Leu Thr  
 50 85 90 95  
 52 aga ttg atg att cct atg atg tct cca att gca gaa att gag gat att 336  
 53 Arg Leu Met Ile Pro Met Met Ser Pro Ile Ala Glu Ile Glu Asp Ile  
 54 100 105 110  
 56 tca gct gct gct tcc aca gta aca gtg gat gcc aga gtg ggc ata tca 384  
 57 Ser Ala Ala Ala Ser Thr Val Thr Val Asp Ala Arg Val Gly Ile Ser  
 58 115 120 125  
 60 acc ggc gtc tcg gct gca gat agg gca aaa acg att ttt act cta gcc 432

p.6

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61	Thr	Gly	Val	Ser	Ala	Ala	Asp	Arg	Ala	Lys	Thr	Ile	Phe	Thr	Leu	Ala	
62		130					135					140					
64	tcc	cct	gat	tct	aag	cca	act	gac	ctc	aga	aga	cca	ggc	cat	ata	ttc	480
65	Ser	Pro	Asp	Ser	Lys	Pro	Thr	Asp	Leu	Arg	Arg	Pro	Gly	His	Ile	Phe	
66	145				150					155					160		
68	cct	cta	aaa	tac	cga	aac	ggg	ggg	gtg	cta	aaa	aga	gct	gga	cat	act	528
69	Pro	Leu	Lys	Tyr	Arg	Asn	Gly	Gly	Val	Leu	Lys	Arg	Ala	Gly	His	Thr	
70				165					170						175		
72	gag	gca	tcc	gtc	gat	ctt	gtc	gcg	ttg	gct	ggc	ttg	cgc	cct	gtg	tct	576
73	Glu	Ala	Ser	Val	Asp	Leu	Val	Ala	Leu	Ala	Gly	Leu	Arg	Pro	Val	Ser	
74			180						185					190			
76	gtc	ctg	tca	acc	gtc	atc	aac	cca	gtg	gat	ggg	tca	atg	gca	gga	atg	624
77	Val	Leu	Ser	Thr	Val	Ile	Asn	Pro	Val	Asp	Gly	Ser	Met	Ala	Gly	Met	
78			195					200					205				
80	cca	gtg	ctg	aaa	cag	atg	gct	ttg	gag	cat	gat	atc	cca	att	gtt	tca	672
81	Pro	Val	Leu	Lys	Gln	Met	Ala	Leu	Glu	His	Asp	Ile	Pro	Ile	Val	Ser	
82		210					215					220					
84	atc	gct	gat	ctc	atc	cgg	tat	aga	agg	aag	agg	gag	aag	ctg	gtg	gaa	720
85	Ile	Ala	Asp	Leu	Ile	Arg	Tyr	Arg	Arg	Lys	Arg	Glu	Lys	Leu	Val	Glu	
86	225				230					235					240		
88	ctg	att	gct	gta	tct	cgt	ttg	ccg	acg	aaa	tgg	ggc	ctt	ttc	cga	gct	768
89	Leu	Ile	Ala	Val	Ser	Arg	Leu	Pro	Thr	Lys	Trp	Gly	Leu	Phe	Arg	Ala	
90				245					250					255			
92	tac	tgc	tac	caa	tcc	aag	ctt	gat	gga	acc	gag	cac	att	gct	gtt	gca	816
93	Tyr	Cys	Tyr	Gln	Ser	Lys	Leu	Asp	Gly	Thr	Glu	His	Ile	Ala	Val	Ala	
94			260						265				270				
96	aag	ggc	gac	atc	ggc	gac	ggc	gag	gac	gtc	ttg	gtg	agg	gtc	cat	tcc	864
97	Lys	Gly	Asp	Ile	Gly	Asp	Gly	Glu	Asp	Val	Leu	Val	Arg	Val	His	Ser	
98			275					280					285				
100	gag	tgc	ctg	acc	ggc	gac	atc	ctc	ggc	tcc	gcc	cgc	tgc	gac	tgc	ggc	912
101	Glu	Cys	Leu	Thr	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Arg	Cys	Asp	Cys	Gly	
102			290				295					300					
104	aac	cag	ctg	gac	ctg	gcg	atg	cag	ctc	atc	gac	aag	gcc	ggc	cgc	ggc	960
105	Asn	Gln	Leu	Asp	Leu	Ala	Met	Gln	Leu	Ile	Asp	Lys	Ala	Gly	Arg	Gly	
106	305				310					315				320			
108	gtc	ctc	gtc	tac	ctc	cgc	ggc	cac	gag	ggc	cgc	ggc	atc	ggc	ctc	ggc	1008
109	Val	Leu	Val	Tyr	Leu	Arg	Gly	His	Glu	Gly	Arg	Gly	Ile	Gly	Leu	Gly	
110				325					330					335			
112	cag	aag	ctc	cgc	gcc	tac	aac	ctc	cag	gac	gac	ggc	cac	gac	acc	gtc	1056
113	Gln	Lys	Leu	Arg	Ala	Tyr	Asn	Leu	Gln	Asp	Asp	Gly	His	Asp	Thr	Val	
114			340						345				350				
116	cag	gcc	aac	gtc	gag	ctc	ggc	ctc	gcc	gtc	gac	tcc	cgc	gag	tac	ggc	1104
117	Gln	Ala	Asn	Val	Glu	Leu	Gly	Leu	Ala	Val	Asp	Ser	Arg	Glu	Tyr	Gly	
118			355					360					365				
120	atc	ggc	gcc	cag	att	ctg	cgg	gac	atg	ggg	gtg	cgc	acg	atg	cgg	ctg	1152
121	Ile	Gly	Ala	Gln	Ile	Leu	Arg	Asp	Met	Gly	Val	Arg	Thr	Met	Arg	Leu	
122			370				375						380				
124	atg	acg	aac	aac	ccg	gca	aag	ttc	gtc	ggg	ctc	aag	ggc	tac	ggg	ctc	1200
125	Met	Thr	Asn	Asn	Pro	Ala	Lys	Phe	Val	Gly	Leu	Lys	Gly	Tyr	Gly	Leu	

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126 385          390          395          400
128 gcc gtc gtc ggc agg gtt ccg gtg atc tcc ccc atc acc aag gag aac      1248
129 Ala Val Val Gly Arg Val Pro Val Ile Ser Pro Ile Thr Lys Glu Asn
130          405          410          415
132 cag agg tac ctc gag acg aag cgc acc aag atg ggc cat gtc tac ggc      1296
133 Gln Arg Tyr Leu Glu Thr Lys Arg Thr Lys Met Gly His Val Tyr Gly
134          420          425          430
136 tcc gac ctc ccc ggc aac gtc ccg gag gaa ttc ctc aac ccg gac gac      1344
137 Ser Asp Leu Pro Gly Asn Val Pro Glu Glu Phe Leu Asn Pro Asp Asp
138          435          440          445
140 atc gcc gga gac caa gac gaa gac gac acc cac aac tga      1383
141 Ile Ala Gly Asp Gln Asp Glu Asp Asp Thr His Asn
142          450          455          460
145 <210> SEQ ID NO: 2
146 <211> LENGTH: 460
147 <212> TYPE: PRT
148 <213> ORGANISM: Oryza sativa
150 <400> SEQUENCE: 2
152 Ala Ser Phe Arg Thr Val Gly Ala Lys Ile Thr Gln Glu Thr Gly Asp
153 1          5          10          15
156 Phe Phe Val Ser Asp Ala Glu Gly Asp Pro Asp Lys Pro Thr Asp Gly
157          20          25          30
160 Phe Ser Ser Ile Asp Glu Ala Ile Gly Ala Leu His Glu Gly Lys Phe
161          35          40          45
164 Val Ile Ala Val Asp Asp Glu Ser Gly Asp Asn Glu Gly Asp Leu Val
165          50          55          60
168 Met Ala Ala Thr Leu Ala Asp Pro Glu Ser Ile Ala Phe Met Ile Arg
169 65          70          75          80
172 Asn Gly Ser Gly Ile Ile Ser Val Gly Met Lys Glu Glu Asp Leu Thr
173          85          90          95
176 Arg Leu Met Ile Pro Met Met Ser Pro Ile Ala Glu Ile Glu Asp Ile
177          100          105          110
180 Ser Ala Ala Ala Ser Thr Val Thr Val Asp Ala Arg Val Gly Ile Ser
181          115          120          125
184 Thr Gly Val Ser Ala Ala Asp Arg Ala Lys Thr Ile Phe Thr Leu Ala
185          130          135          140
188 Ser Pro Asp Ser Lys Pro Thr Asp Leu Arg Arg Pro Gly His Ile Phe
189 145          150          155          160
192 Pro Leu Lys Tyr Arg Asn Gly Gly Val Leu Lys Arg Ala Gly His Thr
193          165          170          175
196 Glu Ala Ser Val Asp Leu Val Ala Leu Ala Gly Leu Arg Pro Val Ser
197          180          185          190
200 Val Leu Ser Thr Val Ile Asn Pro Val Asp Gly Ser Met Ala Gly Met
201          195          200          205
204 Pro Val Leu Lys Gln Met Ala Leu Glu His Asp Ile Pro Ile Val Ser
205          210          215          220
208 Ile Ala Asp Leu Ile Arg Tyr Arg Arg Lys Arg Glu Lys Leu Val Glu
209 225          230          235          240
212 Leu Ile Ala Val Ser Arg Leu Pro Thr Lys Trp Gly Leu Phe Arg Ala

```

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```

213          245          250          255
216 Tyr Cys Tyr Gln Ser Lys Leu Asp Gly Thr Glu His Ile Ala Val Ala
217          260          265          270
220 Lys Gly Asp Ile Gly Asp Gly Glu Asp Val Leu Val Arg Val His Ser
221          275          280          285
224 Glu Cys Leu Thr Gly Asp Ile Leu Gly Ser Ala Arg Cys Asp Cys Gly
225          290          295          300
228 Asn Gln Leu Asp Leu Ala Met Gln Leu Ile Asp Lys Ala Gly Arg Gly
229 305          310          315          320
232 Val Leu Val Tyr Leu Arg Gly His Glu Gly Arg Gly Ile Gly Leu Gly
233          325          330          335
236 Gln Lys Leu Arg Ala Tyr Asn Leu Gln Asp Asp Gly His Asp Thr Val
237          340          345          350
240 Gln Ala Asn Val Glu Leu Gly Leu Ala Val Asp Ser Arg Glu Tyr Gly
241          355          360          365
244 Ile Gly Ala Gln Ile Leu Arg Asp Met Gly Val Arg Thr Met Arg Leu
245          370          375          380
248 Met Thr Asn Asn Pro Ala Lys Phe Val Gly Leu Lys Gly Tyr Gly Leu
249 385          390          395          400
252 Ala Val Val Gly Arg Val Pro Val Ile Ser Pro Ile Thr Lys Glu Asn
253          405          410          415
256 Gln Arg Tyr Leu Glu Thr Lys Arg Thr Lys Met Gly His Val Tyr Gly
257          420          425          430
260 Ser Asp Leu Pro Gly Asn Val Pro Glu Glu Phe Leu Asn Pro Asp Asp
261          435          440          445
264 Ile Ala Gly Asp Gln Asp Glu Asp Asp Thr His Asn
265          450          455          460
268 <210> SEQ ID NO: 3
269 <211> LENGTH: 267
270 <212> TYPE: DNA
271 <213> ORGANISM: Oryza sativa
274 <220> FEATURE:
275 <221> NAME/KEY: CDS
276 <222> LOCATION: (1)..(267)
278 <400> SEQUENCE: 3
279 gga acà aac cct ggc ttc aga gtt gga gag atc agg ctc tcc aac agg      48
280 Gly Thr Asn Pro Gly Phe Arg Val Gly Glu Ile Arg Leu Ser Asn Arg
281 1          5          10          15
283 gat att tat ttc ggc aca tta ttg ggg aac aca cca gag ggt tca ggg      96
284 Asp Ile Tyr Phe Gly Thr Leu Leu Gly Asn Thr Pro Glu Gly Ser Gly
285          20          25          30
287 agg tat gtc tgg tca gat ggt tgc act tac gat ggt gag tgg agg aga      144
288 Arg Tyr Val Trp Ser Asp Gly Cys Thr Tyr Asp Gly Glu Trp Arg Arg
289          35          40          45
291 ggg atg agg cat ggg caa gga aag aca atg tgg cca tct gga gcc acc      192
292 Gly Met Arg His Gly Gln Gly Lys Thr Met Trp Pro Ser Gly Ala Thr
293          50          55          60
295 tac gag ggt gag tac tct ggt ggc tac att tat ggt gaa ggc aca tat      240
296 Tyr Glu Gly Glu Tyr Ser Gly Gly Tyr Ile Tyr Gly Glu Gly Thr Tyr

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297 65              70              75              80
299 acc ggg tct gac aac atc gtc tac aag                267
300 Thr Gly Ser Asp Asn Ile Val Tyr Lys
301              85
304 <210> SEQ ID NO: 4
305 <211> LENGTH: 89
306 <212> TYPE: PRT
307 <213> ORGANISM: Oryza sativa
309 <400> SEQUENCE: 4
311 Gly Thr Asn Pro Gly Phe Arg Val Gly Glu Ile Arg Leu Ser Asn Arg
312 1              5              10              15
315 Asp Ile Tyr Phe Gly Thr Leu Leu Gly Asn Thr Pro Glu Gly Ser Gly
316              20              25              30
319 Arg Tyr Val Trp Ser Asp Gly Cys Thr Tyr Asp Gly Glu Trp Arg Arg
320              35              40              45
323 Gly Met Arg His Gly Gln Gly Lys Thr Met Trp Pro Ser Gly Ala Thr
324              50              55              60
327 Tyr Glu Gly Glu Tyr Ser Gly Gly Tyr Ile Tyr Gly Glu Gly Thr Tyr
328 65              70              75              80
331 Thr Gly Ser Asp Asn Ile Val Tyr Lys
332              85
335 <210> SEQ ID NO: 5
336 <211> LENGTH: 1227
337 <212> TYPE: DNA
338 <213> ORGANISM: Oryza sativa
341 <220> FEATURE:
342 <221> NAME/KEY: CDS
343 <222> LOCATION: (1)..(1227)
345 <400> SEQUENCE: 5
346 cca cgc gtc cgg aga agc ggc cgc ttt ttt ttt ttg ttt tcc cct ccg                48
347 Pro Arg Val Arg Arg Ser Gly Arg Phe Phe Phe Leu Phe Ser Pro Pro
348 1              5              10              15
350 act ccg act ccg atc gat ctc cac ccc gaa tcc ctc ctc ctc acc gcc                96
351 Thr Pro Thr Pro Ile Asp Leu His Pro Glu Ser Leu Leu Leu Thr Ala
352              20              25              30
354 ggc gag ctt ccg gct gcg gcg gag atg gcc aca cgt tat tgg atc gtg                144
355 Gly Glu Leu Pro Ala Ala Ala Glu Met Ala Thr Arg Tyr Trp Ile Val
356              35              40              45
358 tct ctt ccc gtg cag act cct ggc tcc acc gcc aat tct ctc tgg gcg                192
359 Ser Leu Pro Val Gln Thr Pro Gly Ser Thr Ala Asn Ser Leu Trp Ala
360              50              55              60
362 cgc ctc cag gac tcc atc tcg cgc cac tcc ttc gac acg ccg ctc tac                240
363 Arg Leu Gln Asp Ser Ile Ser Arg His Ser Phe Asp Thr Pro Leu Tyr
364 65              70              75              80
366 cgg ttt aac gtc ccc gat ctc cgc gtc ggc acg ctc gac tcc ctc ctc                288
367 Arg Phe Asn Val Pro Asp Leu Arg Val Gly Thr Leu Asp Ser Leu Leu
368              85              90              95
370 gcc ctc agc gac gat ctc gtc aag tcc aac gtc ttc atc gag ggg gtc                336
371 Ala Leu Ser Asp Asp Leu Val Lys Ser Asn Val Phe Ile Glu Gly Val

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; Xaa Pos. 23,56,57,104,126  
Seq#:32; Xaa Pos. 23,56,57,104,126  
Seq#:43; Xaa Pos. 64  
Seq#:44; Xaa Pos. 64  
Seq#:57; Xaa Pos. 34  
Seq#:58; Xaa Pos. 34  
Seq#:71; Xaa Pos. 956,961,1086  
Seq#:72; Xaa Pos. 956,961,1086  
Seq#:81; Xaa Pos. 264  
Seq#:82; Xaa Pos. 264  
Seq#:129; Xaa Pos. 226  
Seq#:130; Xaa Pos. 226  
Seq#:137; Xaa Pos. 2,6  
Seq#:138; Xaa Pos. 2,6

## VERIFICATION SUMMARY

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Input Set : D:\1392-10-20-PCT.ST25.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:3062 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:31  
L:3062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:96  
M:341 Repeated in SeqNo=31  
L:3238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:16  
M:341 Repeated in SeqNo=32  
L:4451 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:43  
L:4451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:192  
L:4543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:48  
L:5699 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:57  
L:5699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:144  
L:5947 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:32  
L:8585 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:71  
L:8585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:2880  
M:341 Repeated in SeqNo=71  
L:8923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:944  
M:341 Repeated in SeqNo=72  
L:9867 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:81  
L:9867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:816  
L:9979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:256  
L:14300 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:129  
L:14300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129 after pos.:720  
L:14380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130 after pos.:224  
L:14973 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:137  
L:14973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:48  
L:15270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:0